Atty. Docket No. 0508-1004 # 7

PATENTS

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of

Gerard GIORDANO et al.

Confirmation No. 8083

Serial No. 10/088,117

BOX PCT

Filed March 15, 2002

NUCLEOTIDE SEQUENCES DERIVED FROM GENES CODING FOR TRIMETHYLAMINE N-OXIDE REDUCTASE, AND USES THEREOF, ESPECIALLY FOR THE DETECTION OF BACTERIA

STATEMENT TO SUPPORT FILING AND SUBMISSION IN ACCORDANCE WITH 37 C.F.R. §§ 1.821-1.825

Commissioner for Patents

Washington, D.C. 20231

Sir:

Responsive to the Official Action of May 20, 2002, a Sequence Listing is submitted concurrently herewith.

The undersigned hereby states that:

- the submission, filed herewith in accordance with
 C.F.R. § 1.821(g), does not include new matter;
- 2. the content of the attached paper copy and the attached computer readable copy of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same; and
- 3. all statements made herein of their own knowledge are true and that all statements made on information and belief are believed to be true; and further, that these statements were made with the knowledge that willful false statements and the

GIORDANO et al. S.N. 10/088,117

like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent resulting therefrom.

Respectfully submitted,

YOUNG & THOMPSON

Andrew J. Patch

Attorney for Applicants Registration No. 32,925 745 South 23rd Street Arlington, VA 22202

Telephone: 521-2297

July 22, 2002

1

SEQUENCE LISTING

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<210> 8 <211> 404 <212> PRT

<213> Rhodobacter sphareroides

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50 55 60

His Ser Met Arg Asp Asn Asn Tyr Glu Glu Tyr Lys Thr Thr Ile His 65 70 75 80

Tyr Gln Asn Thr Ser Gly Val Arg Ala Glu Cys Ala Asp Cys His Val

Pro Lys Ser Gly Trp Lys Leu Tyr Arg Ala Lys Leu Leu Ala Ala Lys 100 105 110

Asp Leu Trp Gly Glu Ile Arg Gly Thr Ile Asp Thr Arg Glu Lys Phe 115 120 125

Glu Ala His Arg Leu Glu Met Ala Glu Thr Val Trp Ala Asp Met Lys 130 135 140

Ala Asn Asp Ser Ala Thr Cys Arg Thr Cys His Ser Phe Glu Ala Met 145 150 155 160

Asp Phe Ala His Gln Lys Pro Glu Ala Ser Lys Gln Met Gln Gln Ala 165 170 175

Met Asn Glu Gly Gly Thr Cys Ile Asp Cys His Lys Gly Ile Ala His 180 185 190 Lys Met Pro Asp Met Ala Ser Gly Tyr Arg Ala Leu Phe Ser Lys Leu Glu Lys Ala Ser Gln Ser Leu Lys Pro Arg Lys Gly Glu Thr Leu Tyr 215 Pro Leu Arg Thr Ile Glu Ala Tyr Leu Glu Lys Pro Ser Gly Glu Lys Ala Lys Ala Asp Gly Arg Leu Leu Ala Ala Thr Pro Met Gln Val Val Asp Val Thr Gly Asp Trp Val Gln Val Ala Val Lys Gly Trp Gln Gln 265 Glu Gly Ala Glu Arg Val Ile Tyr Glu Lys Gln Gly Lys Arg Ile Phe Asn Ala Ala Leu Ala Pro Ala Ala Thr Gly Ser Val Val Pro Gly Ala 295 Ser Met Val Asp Pro Asp Thr Glu Gln Thr Trp Thr Asp Val Ser Leu Thr Ala Trp Val Arg Asn Arg Asp Leu Thr Gly Asp Gln Glu Ala Leu 330 325 Trp Gln Tyr Gly Lys Gln Met Tyr Asn Gly Ala Cys Gly Met Cys His Val Leu Pro His Pro Glu His Phe Leu Ala Asn Gln Trp Ile Gly Thr Leu Asn Ala Met Lys Ser Arg Ala Pro Leu Asp Asp Glu Gln Phe Arg 375 Leu Val Gln Arg Tyr Val Gln Met His Ala Lys Asp Val Glu Pro Glu 395 385

Gly Ala Ala Glu

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ctgaaacgca tctggcagga agggagccag cagggaaaag gtcgcggtat ccacttaccg 180
attttcgagg tgttctggaa tcaacaggag tacatcgagt ttgatcatcc gcagatgttt 240
gtacgccatc aggettteeg tgaagateeg gaeetggage egttgggeae geeaageggt 300
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<210> 11

<211> 390

<212> PRT

<213> Escherichia coli

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- Val Leu Pro His Val Gly Ile Lys Val Thr Ser Thr Thr Glu Phe Cys 35 40 45
- Val Ser Cys His Ser Met Gln Pro Val Tyr Glu Glu Tyr Lys Gln Ser 50 55 60
- Val His Phe Gln Asn Ala Ser Gly Val Arg Ala Glu Cys His Asp Cys 65 70 75 80
- His Ile Pro Pro Asp Ile Pro Gly Met Val Lys Arg Lys Leu Glu Ala 85 90 95
- Glu Lys Phe Glu Ala Lys Arg Ala Leu Leu Ala Glu Arg Glu Trp Ala 115 120 125
- Arg Met Lys Glu Asn Asn Ser Ala Thr Cys Arg Ser Cys His Asn Tyr 130 135 140
- Asp Ala Met Asp His Ala Lys Gln His Pro Glu Ala Ala Arg Gln Met 145 150 150 155
- Lys Val Ala Ala Lys Asp Asn Gln Ser Cys Ile Asp Cys His Lys Gly 165 170
- Ile Ala His Gln Leu Pro Asp Met Ser Ser Gly Phe Arg Lys Gln Phe 180 185 190
- Asp Asp Val Arg Ala Ser Ala Asn Asp Ser Gly Asp Thr Leu Tyr Ser 195 200 205
- Ile Asp Ile Lys Pro Ile Tyr Ala Ala Lys Gly Asp Lys Glu Ala Ser 210 225 220
- Gly Ser Leu Leu Pro Ala Ser Glu Val Lys Val Leu Lys Arg Asp Gly 225 230 235
- Asp Trp Leu Gln Ile Glu Ile Thr Gly Trp Thr Glu Ser Ala Gly Arg 245 250 255
- Gln Arg Val Leu Thr Gln Phe Pro Gly Lys Arg Ile Phe Val Ala Ser 260 265 270
- Ile Arg Gly Asp Val Gln Gln Gln Val Lys Thr Leu Glu Lys Thr Thr 275 280 285
- Val Ala Asp Thr Asn Thr Glu Trp Ser Lys Leu Gln Ala Thr Ala Trp 290 295 300
- Met Lys Lys Gly Asp Met Val Asn Asp Ile Lys Pro Ile Trp Ala Tyr 305 310 315 320

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Glu Ile Ala His Phe Asp Ala Asn Gly Trp Ile Gly Thr Leu Asn Gly
Met Ile Gly Phe Thr Ser Leu Asp Lys Arg Glu Glu Arg Thr Leu Leu
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Lys Tyr Leu Gln Met Asn Ala Ser Asp Thr Ala Gly Lys Ala His Gly
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Asp Lys Lys Glu Glu Lys
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<213> Artificial sequence

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